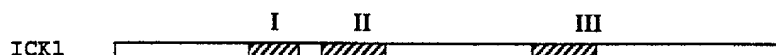


A



B

ATCTCTCTCTCTCACAGAGATTGTAACCTTACGCACACGTAACCTAAATCGAAGATGGTG 60
 M V 2
 AGAAAATATAGAAAAGCTAAAGGAATTGTAGAAGCTGGAGTTTCGTCAACGTATATGCAG 120
 R K Y R K A K G I V E A G V S S T Y M Q 22
 CTACGGAGCCGGAGAATTGTTTATGTTAGATCGGAAAAATCAAGCTCTGTCTCCGTCGTC 180
 L R S R R I V Y V R S E K S S S V S V V 42
 GGTGATAATGGAGTTTCGTCTCTTGTAGTGAAGCAATGAATATAAGAAGAAAGAATTA 240
 G D N G V S S S C S G S N E Y K K K E L 62
 VI VII
 ATACATCTGGAGGAGGAAGATAAAGATGGTGACACTGAAACGTCGACGTATCGACGGGGT 300
 I H L E E E D K D G D T E T S T Y R R G 82
 ACGAAGAGGAAGCTTTTGTAAAATCTGAGAGAGGAGGAGAAAGAAGAAATTAAGTAAATCC 360
 T K R K L F E N L R E E E K E E L S K S 102
 ATGGAGAATTATTCATCGGAATTTGAATCGGCGGTAAAGAATCGTTAGATTGTTGTTGT 420
 M E N Y S S E F E S A V K E S L D C C C 122
 AGCGGGAGGAAAACGATGGAGGAGACGGTGACGCGGAGGAGGAGGAGAAGCGGAAATTG 480
 S G R K T M E E T V T A E E E E K A K L 142
 ATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTGTGGAAGCTGAGAAACAA 540
 M T E M P T E S E I E D F F V E A E K Q 162
 VIII
 CTCAAAGAAAAATTCAAGAAGAAGTACAATTTTCGATTTCGAGAAGGAGAAGCCATTAGAA 600
 L K E K F K K K Y N F D F E K E K P L E 182
 GGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTATGGTTTTTTTTT 660
 G R Y E W V K L E . 191
 TAACCTTTTAGATTTTAATATTTTCAGGGAATAAGTTAATTTTATTTTGTGATTGGAAA 720
 TATAAGATTTGTAGGAGGAATGTTTTTAGAAGTACGAAATTGCACAGA^{*}AAAAGA^{*}AGAAAG 780
 CTTTTTAACAGAT^{*}TTTAGAGCCCAGAA^{*}AAGTCGTGTCTTTTAGCTCTACTTTTACCTCTT 840
 CTTGGAATCTTGTGTATCTTTTAGCATATTCTTTAGTACAT^{*}TTTTATGTTTTTGGTGA^{*}CT 900
 GATA^{*} 905

Characterization of cDNA (Wang et al., 1997) and genomic sequences of *ICK1*.
 (A). Genomic organization *ICK1*. Open bars represent exons and filled bars, introns.
 (B). Features of cDNA sequence and deduced amino acid sequence.

Figure 1

61 ACGTATATGCAGCTACGGAGCCGGAGAATTGTTTATGTTAGATCGGAAAAATCAAGCTCT Ick1.seq
 3 ACGTATATGCAGCTACGGAGCCGGAGAATTGTTTATGTTAGATCGGAAAAATCAAGCTCT ICK1b.seq
 6 GATTGTTT TAG ICK1c.seq

121 GTCTCCGTCGTCGGTGATAATGGAGTTTCGTCGCTTGTAGTGGGAAGCAATGAATATAAG Ick1.seq
 63 GTCTCCGTCGTCGGTGATAATGGAG ICK1b.seq
 18 ICK1c.seq

181 AAGAAAGAATTAATACATCTGGAGGAGGAAGATAAAGATGGTGACACTGAAACGTCGACG Ick1.seq
 88 ICK1b.seq
 18 ICK1c.seq

241 TATCGACGGGTACGAAGAGGAAGCTTTTGAATCTGAGAGAGGAGGAGAAAGAAGAA Ick1.seq
 88 ICK1b.seq
 18 GGGTACGAAGAGGAAGCTTTTGAATCTGAGAGAGGAGGAGAAAGAAGAA ICK1c.seq

301 TTAAGTAAATCCATGGAGAATTATTCATCGGAATTTGAATCGGCGGTTAAGAATCGTTA Ick1.seq
 88 AATTATTCATCGGAATTTGAATCGGCGGTTAAGAATCGTTA ICK1b.seq
 70 TTAAGTAAATCCATGGAGAATTATTCATCGGAATTTGAATCGGCGGTTAAGAATCGTTA ICK1c.seq

361 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAG Ick1.seq
 130 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAG ICK1b.seq
 130 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAG GAGGAG ICK1c.seq

421 AAGGCGAAATTGATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTGTGGAA Ick1.seq
 190 AAGGCGAAATTGATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTGTGGAA ICK1b.seq
 172 AAGGCGAAATTGATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTGTGGAA ICK1c.seq

461 GCTGAGAAACAACCTCAAAGAAAAATTCAAGAAGAAGTACAATTCGATTTCGAGAAGGAG Ick1.seq
 250 GCTGAGAAACAACCTCAAAGAAAAATTCAAGAAGAAGTACAATTCGATTTCGAGAAGGAG ICK1b.seq
 232 GCTGAGAAACAACCTCAAAGAAAAATTCAAGAAGAAGTACAATTCGATTTCGAGAAGGAG ICK1c.seq

541 AAGCCATTAGAAGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTA Ick1.seq
 310 AAGCCATTAGAAGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTA ICK1b.seq
 292 AAGCCATTAGAAGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTA ICK1c.seq

601 TGGTTTTTTTTTAACTTTTATAGATTTTAATATTTTCAGGGAATAAGTTAATTTTATTTTG Ick1.seq
 370 TGGTTTTTTTTTAACTTTTATAGATTTTAATATTTTCAGGGAATAAGTTAATTTTATTTTG ICK1b.seq
 352 TGGTTTTTTTTTAACTTTTATAGATTTT ICK1c.seq

661 TTGATTGGAATATAAGATTTGTAGGAGGAATGTTTTAGAAAGTACGAAATTGCACAGA Ick1.seq
 430 TTGATTGGAATATA ICK1b.seq
 379 ICK1c.seq

Alignment of *ICK1* cDNA sequence with *ICK1b* and *ICK1c* showing the differences

Figure 2

GTGGAATCTAGGATAATTCTGTCTCCGTGTGTACAGGCGACGAATCGCGGTGGAATTGTG
GCGAGAAATTCAGCAGGAGCGTCGGAGACGAGTGTGTTATAGTACGACGGCGAGATTCT
CCTCCGGTTGAAGAACAGTGTCAAATCGAAGAAGAAGATTCTGTCGGTTTCGTGTTGTTCT
ACATCGGAAGAGAAATCGAAACGGAGAATCGAATTTGTAGATCTTGAGGAAAATAACGGT
GACGATCGTGAAACAGAAACGTCGTGGATTTACGATGATTTGAATAAGAGTGAGGAATCG
ATGAACATGGATTCTTCTTCGGTGGCTGTTGAAGATGTAGAGTCTCGCCGCAGGTTAAGG
AAGAGTCTCCATGAGACGGTGAAGGAAGCTGAGTTAGAAGACTTTTTTCAGGTGGCGGAG
AAAGATCTTCGGAATAAGTTGTTGGAATGTTCTATGAAGTATAACTTCGATTTTCGAGAAA
GATGAGCCACTTGGTGGAGGAAGATACGAGTGGGTAAATTGAATCCATGAAGAAGACGA
TGATGATAATGATGATCATTGTTTTACCAAAGTACTTATTATTTCTTCTGTATAAT
CTTTGCTTTGATTTTTCTTTTAACAAAATCCAAATGTAGATATCTTCTCTCGAATAATC
AATAACATGTAATCAACTTTTGTGTTGTAATTCCTTGAGGTAATTAATTAGATTCGTGTT
TTTCTCGATTAATAAACTATAAGTTTATAACTAAA

cDNA sequence of *ICK2*

Figure 3

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cDNA sequence of *ICN2*

4/8

cDNA sequence of ICN6

5/8

[illegible]

ATTAAAGAGTCTGGTTCAGGTCTCGCGTTGACTCGGTTAACTCGGCTCCTGTAGCTCAG
 AGCTCTAATGAAGATGAATGTTTTGACAATTCGTGAGTGTCCAAGTTTCTTGTTGGTGAA
 AACAGTCTCGGTTTTGAATCAAGACACAGCACAAGGGAGAGCACGCCTTGTAACTTTGT
 GAGGATATGGAGATCATGGTTACACCAGGGTCTAGCACGAGGTCGATGTGCAGAGCAACC
 AAAGAGTACACAAGGGAACAAGATAACGTGATCCCGACCACTAGTGAAATGGAGGAGTTC
 TTTGCATATGCAGAGCAGCAGCAACAGAGGCTATTATGGAGAAGTACAACCTCGACATT
 GTGAATGATATCCCCCTCAGCGGACGTTACGAATGGGTGCAAGTCAAACCATGAAGTTCA
 AAAGGAAACAGCTCCAAAAGACATGGTGTGAAGTTAGAGAATTGTGATGGAGTTAACAG
 AACTAACCAACATCAGAAATCGTGTTAATCCTTAAGTTAATAATGTGGGTAA

cDNA sequence of *ICN7*

**SEQ ID NO. 15: The nucleotide sequence of *Chenopodium rubrum* CDKII
 (GenBank AJ002173)**

gcacgagcgaaattcggtgtaggaggttaaaccagagctcgagactgccctagctatggcggcagctgctactcaac
 ttcgtcicccggcgaagaagatcaagaaggttcgaagtcgtctataatattcctcaactaagaagtcgtcgaagaatt
 tgcggcgccggagaatttcgccgaattagaaacgacgccgttggaagttgcggcggttgtaggaggaagaggttgcg
 aattgctcgagtagcgaagtaattactacagctaggtcggatttccgcccgtctgttgcgaagcaattatgatcagtt
 gaggctcagcagccagaagtagttaaggatgatgatggttgggaaatcgtacagcagatccagaggttgagagtggtg
 aggcgtcgtcaaagcaaaaggagagccatagaacagaagcagagagaagctacaaaattagacgaccaggattatccggcg
 acgaaatcaacggtacagatcaagatgccgtctgattcagaatcgaagaattcttgcgtgtgctgaaaaagatctcca
 gaaacgcttcagcgaaaagtacaatttcacatagttaaggacgtgccactgaaaggtcggttatgattgggtccaataa
 atccatgaataaaaccactggtgatagtgatgatgaatgactgaattctccacaattacgcaaaattagccact
 gaaattgcaaaagtaaatcttaatttagcctttcttcttttagcagaagtgatctattctcacaccgaaaaaaaa
 aaaa

SEQ ID NO. 16: The amino acid sequence of *Chenopodium rubrum* CDKI1
 MAAAATPTSS PAKKIKKVSK SSYNIPQLRS RRKNLSAPEN FAELETTPL
 VAAVVEEEVANCSSSEVIT TARSDFPSC CSSNYDQLSS SEPEVVKDDD
 GLGNRTADPE VESGEASSKQ KESHRTEARE ATKLDDQDYP ATKSTVQIKM
 PSDSEIEEFF AVAEKDLQKR FSEKYNFDIV KDVPLKGRYD WVPINP

Figure 6

	V...S.S.V...C.....E....S.S	Consensus
1	MVRKYRKA-----KGIVEAGVSSVTYMLRSRRIV---YYRSEKSSSVWVDNGVSSCGSGSNEYKKELIHLFEEDKDGD	ICK1.pro
1	V-----ESRIILSPCVQATNRGGIVARNAGA-----SETSVIVRRRDSPPV-----EEQ-----QISEEDSVV	ICK2.pro
1	KKQREPAHKNPREKKMSERKRELAEALSTSFPLKTKINDSSDSDPSHDVIFAVSSVASAALASDESVTIGGESDQ-SS	ICN2.pro
1	LS--PEKTIMSLREMSETPKRDSYEGLN-----IKMRLDDDDDLRSPRTLIS-SSSSSLAYVDSGGFVSVALSEEEDHLS	ICN6.pro
1	IKESGSRDVD-----VNMPVAOSNEDEDFDNFV-----	ICN7.pro
	C.SE.K-.F.DLE.....E.L.E.....F.K.....R.....K.K.....PT.AE.E	Consensus
74	TETSTYRGTT-----RKLCENREEEKEELSKSMENYSSEL---ESAVKS-DCCCSGRKTMTEETV-TAEETEAKLMTMEESTIE	ICK1.pro
58	--CSTPHE-----SKRRIE-VENNNGDDRRTETSWIYDDLNSEESM--NMDSSSVAVEDVESRR-----LRSLHETVKEL	ICK2.pro
90	ISSGFTHSIAKNSSSGVLDHQIETTETSTFITSNRETSPVSGGTITTEMESSATK-----KQPGVRKTEAAFI	ICN2.pro
83	ISSGSSTNELIATRLP-S-AHEI-STETISTLLTNRRQGISSSENGETA-EMDATTENKDKMEKSPQALD	ICN6.pro
34	VQVSGEN-----SLGF SRHSSTRSIPCNFV-----DM-IIMVTPGSTSRMCRAKEYTREQDNVIITSM	ICN7.pro
	DEF..AE.-.Q....F.E---KYNFDIVND.PLEG-RYEWV.L.P-	Consensus
154	VEEK--LKEK-KK-----FEKEK-----KKE	ICK1.pro
134	QVKK--DLRNKLKCSM-----FEKEK-----GCKKKN.	ICK2.pro
174	LSELQDDKKKCII-----K-----K-----DRL	ICN2.pro
169	SARVEKCR--TI-----Y-----QSK-	ICN6.pro
	SVYV-----OVK	ICN7.pro

Consensus 'Consensus #1': When 60% (3) match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with black at 40% fill) residues that match the consensus named 'Consensus #1' exactly.

Alignment of deduced amino acid sequences of *ICK1*, *ICK2*, *ICN2*, *ICN6* and *ICN7*

